



ENTERED

PCT10

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/049,182

DATE: 02/25/2002

TIME: 10:48:27

Input Set : A:\36667.txt

Output Set: N:\CRF3\02252002\J049182.raw

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4 <110> APPLICANT: Banks, William A.
6 <120> TITLE OF INVENTION: MODULATION OF THE BLOOD-BRAIN BARRIER TRANSPORTER FOR
7   LEPTIN
9 <130> FILE REFERENCE: 01017/35040
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/049,182
C--> 12 <141> CURRENT FILING DATE: 2002-02-08
14 <160> NUMBER OF SEQ ID NOS: 6
16 <170> SOFTWARE: PatentIn Ver. 2.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 2793
20 <212> TYPE: DNA
21 <213> ORGANISM: Murine
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Murine ob (leptin) cDNA
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (57)..(557)
30 <220> FEATURE:
31 <221> NAME/KEY: sig_peptide
32 <222> LOCATION: (57)..(59)
34 <220> FEATURE:
35 <221> NAME/KEY: mat_peptide
36 <222> LOCATION: (60)..(557)
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39 ggatccctgc tccagcagct gcaaggtgca agaagaagaa gatcccaggg aggaaa atg 59
40                                     Met
41                                     -1
43 tgc tgg aga ccc ctg tgt cgg ttc ctg tgg ctt tgg tcc tat ctg tct 107
44 Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu Ser
45   1           5           10           15
47 tat gtt caa gca gtg cct atc cag aaa gtc cag gat gac acc aaa acc 155
48 Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr
49   20           25           30
51 ctc atc aag acc att gtc acc agg atc aat gac att tca cac acg cag 203
52 Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln
53   35           40           45
56 tcg gta tcc gcc aag cag agg gtc act ggc ttg gac ttc att cct ggg 251
57 Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly
58   50           55           60
60 ctt cac ccc att ctg agt ttg tcc aag atg gac cag act ctg gca gtc 299
61 Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val
62   65           70           75           80
64 tat caa cag gtc ctc acc agc ctg cct tcc caa aat gtg ctg cag ata 347

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65 Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile
66                               85                               90                               95
68 gcc aat gac ctg gag aat ctc cga gac ctc ctc cat ctg ctg gcc ttc 395
69 Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe
70                               100                               105                               110
72 tcc aag agc tgc tcc ctg cct cag acc agt ggc ctg cag aag cca gag 443
73 Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu
74                               115                               120                               125
76 agc ctg gat ggc gtc ctg gaa gcc tca ctc tac tcc aca gag gtg gtg 491
77 Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val
78                               130                               135                               140
80 gct ttg agc agg ctg cag ggc tct ctg cag gac att ctt caa cag ttg 539
81 Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu
82 145                               150                               155                               160
84 gat gtt agc cct gaa tgc tgaagtttca aaggccacca ggctcccaag 587
85 Asp Val Ser Pro Glu Cys
86                               165
88 aatcatgtag agggaagaaa ccttggcttc caggggtctt caggagaaga gagccatgtg 647
90 cacacatcca tcattcattt ctctccctcc tgtagaccac ccatccaaag gcatgactcc 707
92 acaatgcttg actcaagtta tccacacaac ttcatgagca caaggagggg ccagcctgca 767
94 gaggggactc tcacctagtt cttcagcaag tagagataag agccatccca tcccctccat 827
96 gtcccacctg ctccgggtac atgttcctcc gtgggtacac gcttcgctgc ggcccaggag 887
98 aggtgaggta gggatgggta gagcctttgg gctgtctcag agtctttggg agcaccgtga 947
100 aggctgcatc cacacacagc tggaaactcc caagcagcac acgatggaag cacttattta 1007
102 ttatttctgc attctatttt ggatggatct gaagcaaggc atcagctttt tcaggctttg 1067
104 ggggtcagcc aggatgagga aggctcctgg ggtgctgctt tcaatcctat tgatgggtct 1127
106 gcccagggca aacctaattt ttgagtgact ggaaggaagg ttgggatctt ccaaacaaga 1187
108 gtctatgcag gtagcgctca agattgacct ctggtgactg gttttgtttc tattgtgact 1247
110 gactctatcc aaacacgttt gcagcggcat tgccgggagc ataggctagg ttattatcaa 1307
112 aagcagatga attttgtcaa gtgtaatatg tatctatgtg cacctgaggg tagaggatgt 1367
114 gttagaggga ggggtgaagga tccggaagtg ttctctgaat tacatatgtg tggtaggctt 1427
116 ttctgaaagg gtgaggcatt ttcttacctc tgtggccaca tagtgtggct ttgtgaaaag 1487
118 gacaaaggag ttgactcttt ccggaacatt tggagtgtac caggcaccct tggaggggct 1547
120 aaagctacag gccttttgtt ggcataattgc tgagctcagg gagtgaaggc cccacatttg 1607
122 agacagttag ccccaagaaa agggtccttg gtgtagatct ccaaggttgt ccagggttga 1667
124 tctcacaatg cgtttcttaa gcaggtagac gtttgcatgc caatatgtgg ttctcatctg 1727
126 attggttcat ccaaagtaga accctgtctc ccacccattc tgtggggagt tttgttccag 1787
128 tgggaatgag aaatcactta gcagatggtc ctgagccctg ggccagcact gctgaggaag 1847
130 tgccagggcc ccaggccagg ctgccagaat tgcccttcgg gctggaggat gaacaaaggg 1907
132 gcttgggttt ttccatcacc cctgcaccct atgtcaccat caaactgggg ggcagatcag 1967
134 tgagaggaca cttgatggaa agcaatacac tttaagactg agcacagttt cgtgctcagc 2027
136 tctgtctggt gctgtgagct agagaagctc accacataca tataaaaaatc agaggctcat 2087
138 gtccctgtgg tttagacccta ctgcggcgcg tgtactccac cacagcagca ccgcaccgct 2147
140 ggaagtacag tgctgtcttc aacaggtgtg aaagaacctg agctgagggg gacagtggcc 2207
142 aggggaaccc tgcttgcatg ctattgcatt tacataccgc atttcagggc acattagcat 2267
144 ccactcctat ggtagcacac tggtgacaat aggacaaggg ataggggttg actatccctt 2327
146 atccaaaatg cttgggacta gaagagtttt ggattttaga gtcttttcag gcataggtat 2387
148 atttgagtat atataaaatg agatatcttg gggatggggc ccaagtataa acatgaagtt 2447
150 catttatatt tcataatacc gtatagacac tgcttgaagt gtagttttat acagtgtttt 2507

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152 aaataacggtt gtatgcatga aagacgtttt tacagcatga acctgtctac tcatgccagc 2567
154 actcaaaaac cttgggggttt tggagcagtt tggatcttgg gttttctgtt aagagatggt 2627
156 tagcttatac ctaaaacat aatggcaaac aggtgcagg accagactgg atcctcagcc 2687
158 ctgaagtgtg ccttccagc caggtcatac cctgtggagg tgagcgggat caggttttgt 2747
160 ggtgctaaga gaggagtgg aggtagattt tggaggatct gagggc 2793
163 <210> SEQ ID NO: 2
164 <211> LENGTH: 167
165 <212> TYPE: PRT
166 <213> ORGANISM: Murine
168 <400> SEQUENCE: 2
169 Met Cys Trp Arg Pro Leu Cys Arg Phe Leu Trp Leu Trp Ser Tyr Leu
170 -1 1 5 10 15
172 Ser Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
173 20 25 30
175 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
176 35 40 45
178 Gln Ser Val Ser Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro
179 50 55 60
181 Gly Leu His Pro Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala
182 65 70 75
184 Val Tyr Gln Gln Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln
185 80 85 90 95
187 Ile Ala Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala
188 100 105 110
190 Phe Ser Lys Ser Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro
191 115 120 125
193 Glu Ser Leu Asp Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val
194 130 135 140
196 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln
197 145 150 155
199 Leu Asp Val Ser Pro Glu Cys
200 160 165
203 <210> SEQ ID NO: 3
204 <211> LENGTH: 700
205 <212> TYPE: DNA
206 <213> ORGANISM: Homo sapiens
208 <220> FEATURE:
209 <221> NAME/KEY: CDS
210 <222> LOCATION: (46)..(546)
212 <220> FEATURE:
213 <221> NAME/KEY: sig_peptide
214 <222> LOCATION: (46)..(48)
216 <220> FEATURE:
217 <221> NAME/KEY: mat_peptide
218 <222> LOCATION: (49)..(546)
220 <220> FEATURE:
221 <223> OTHER INFORMATION: Human ob (leptin) where N represents adenine or
222 guanine or cytosine or thymine
224 <400> SEQUENCE: 3

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W--> 225 nnnngnngttg caaggcccaa gaagcccann ntcctgggaa ggaaa atg cat tgg gga 57
      226                                     Met His Trp Gly
      227                                     -1  1
      229 acc ctg tgc gga ttc ttg tgg ctt tgg ccc tat ctt ttc tat gtc caa 105
      230 Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu Phe Tyr Val Gln
      231      5      10      15
      233 gct gtg ccc atc caa aaa gtc caa gat gac acc aaa acc ctc atc aag 153
      234 Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
      235 20      25      30      35
      237 aca att gtc acc agg atc aat gac att tca cac acg cag tca gtc tcc 201
      238 Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
      239      40      45      50
      241 tcc aaa cag aaa gtc acc ggt ttg gac ttc att cct ggg ctc cac ccc 249
      242 Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
      243      55      60      65
      245 atc ctg acc tta tcc aag atg gac cag aca ctg gca gtc tac caa cag 297
      246 Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
      247      70      75      80
      249 atc ctc acc agt atg cct tcc aga aac gtg atc caa ata tcc aac gac 345
      250 Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile Ser Asn Asp
      251      85      90      95
      253 ctg gag aac ctc cgg gat ctt ctt cac gtg ctg gcc ttc tct aag agc 393
      254 Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser
      255 100      105      110      115
      257 tgc cac ttg ccc tgg gcc agt ggc ctg gag acc ttg gac agc ctg ggg 441
      258 Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
      259      120      125      130
      261 ggt gtc ctg gaa gct tca ggc tac tcc aca gag gtg gtg gcc ctg agc 489
      262 Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser
      263      135      140      145
      265 agg ctg cag ggg tct ctg cag gac atg ctg tgg cag ctg gac ctc agc 537
      266 Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser
      267      150      155      160
W--> 269 cct ggg tgc tgaggccttg aaggctactc ttcttgcaag gactnacgtt 586
      270 Pro Gly Cys
      271      165
      272 aaggggaagga actctggttt ccaggatatct ccaggattga agagcattgc atggacaccc 646
      274 cttatccagg actctgtcaa tttccctgac tcctctaagc cactcttcca aagg 700
      277 <210> SEQ ID NO: 4
      278 <211> LENGTH: 167
      279 <212> TYPE: PRT
      280 <213> ORGANISM: Homo sapiens
      282 <400> SEQUENCE: 4
      283 Met His Trp Gly Thr Leu Cys Gly Phe Leu Trp Leu Trp Pro Tyr Leu
      284 -1  1      5      10      15
      286 Phe Tyr Val Gln Ala Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys
      287      20      25      30
      289 Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr
      290      35      40      45

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TIME: 10:48:27

Input Set : A:\36667.txt

Output Set: N:\CRF3\02252002\J049182.raw

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292 Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro
293      50      55      60
295 Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala
296      65      70      75
298 Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln
299      80      85      90      95
301 Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala
302      100      105      110
304 Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu
305      115      120      125
307 Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val
308      130      135      140
310 Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln
311      145      150      155
313 Leu Asp Leu Ser Pro Gly Cys
314 160      165

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317 &lt;210&gt; SEQ ID NO: 5

318 &lt;211&gt; LENGTH: 146

319 &lt;212&gt; TYPE: PRT

320 &lt;213&gt; ORGANISM: Mus musculus

322 &lt;220&gt; FEATURE:

323 &lt;223&gt; OTHER INFORMATION: Mature mouse ob (leptin)

325 &lt;400&gt; SEQUENCE: 5

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326 Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys Thr
327      1      5      10      15
329 Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser Ala
330      20      25      30
332 Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro Ile
333      35      40      45
335 Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln Val
336      50      55      60
338 Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp Leu
339      65      70      75      80
341 Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser Cys
342      85      90      95
344 Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp Gly
345      100      105      110
347 Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser Arg
348      115      120      125
350 Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser Pro
351      130      135      140
353 Glu Cys
354 145

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357 &lt;210&gt; SEQ ID NO: 6

358 &lt;211&gt; LENGTH: 146

359 &lt;212&gt; TYPE: PRT

360 &lt;213&gt; ORGANISM: Homo sapiens

362 &lt;220&gt; FEATURE:

363 &lt;223&gt; OTHER INFORMATION: Mature human ob (leptin)

## VERIFICATION SUMMARY

PATENT APPLICATION: US/10/049,182

DATE: 02/25/2002

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Input Set : A:\36667.txt

Output Set: N:\CRF3\02252002\J049182.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3

L:269 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3